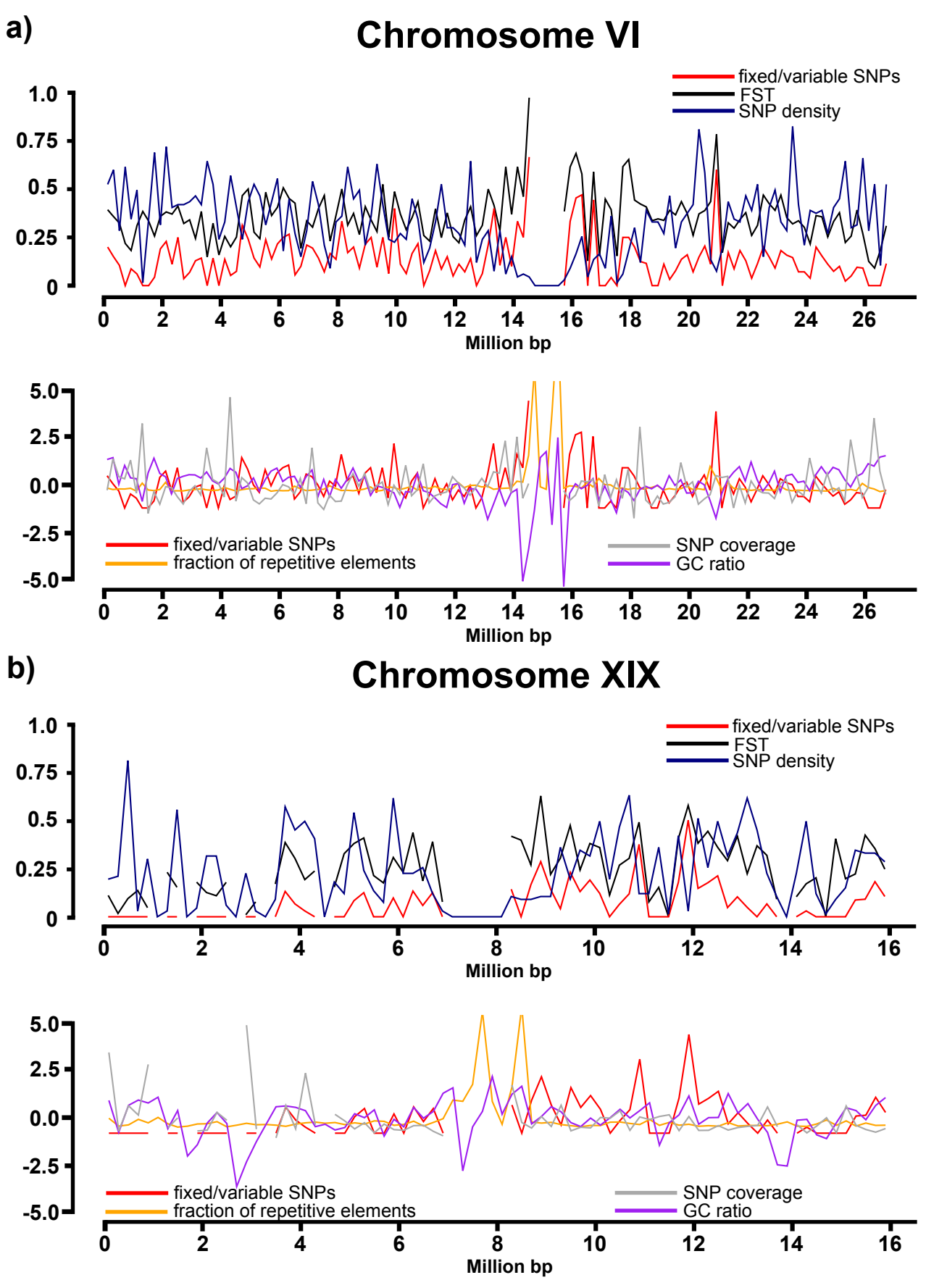
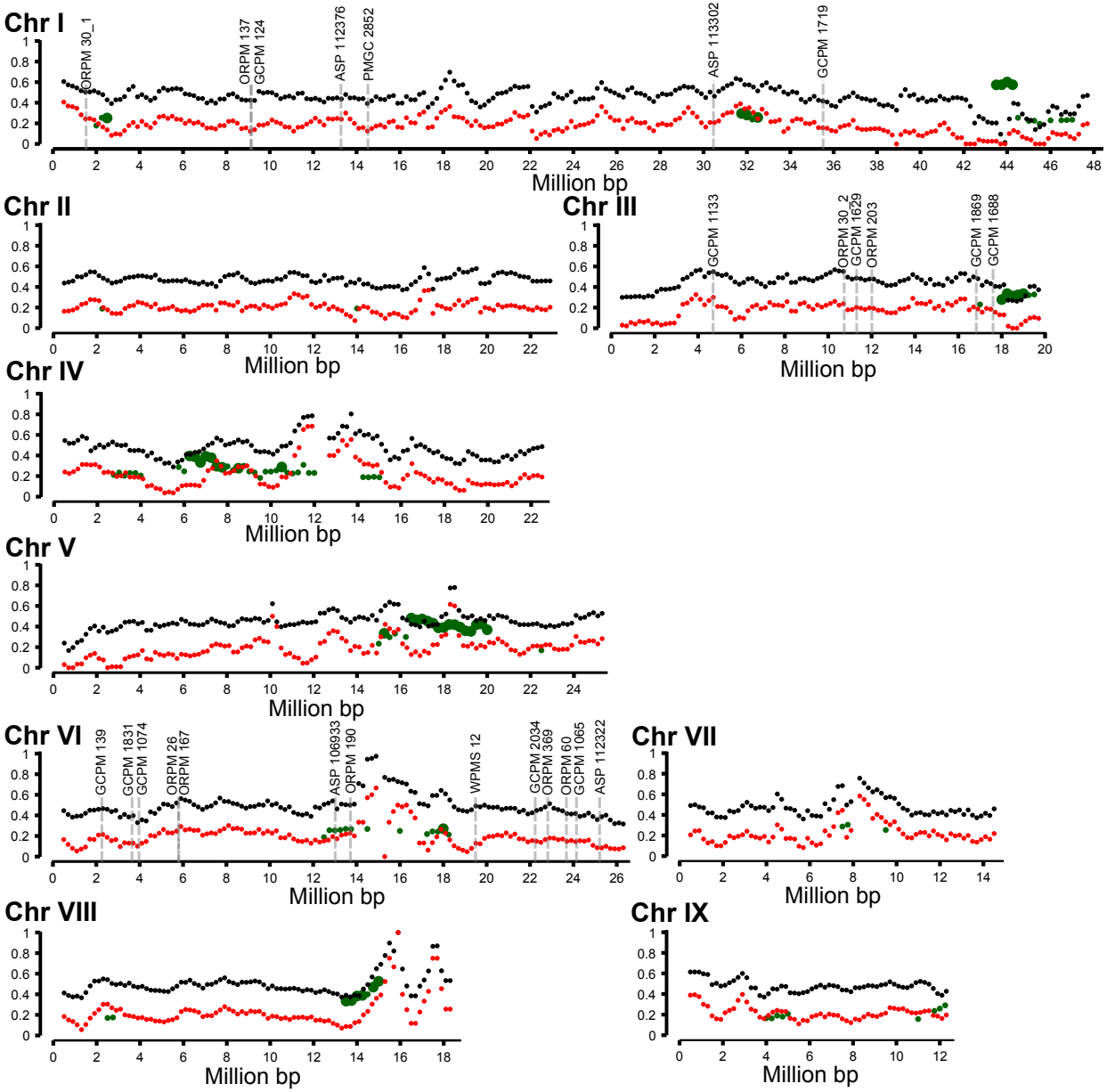

a)
Chromosome VI
fixed/variable SNPs
FST
SNP density
1.0
0.75
0.5
0.25
0
0 2 4 6 8 10 12 14 16 18 20 22 24 26
Million bp
5.0
2.5
0.0
-2.5
-5.0
fixed/variable SNPs
fraction of repetitive elements
SNP coverage
GC ratio
0 2 4 6 8 10 12 14 16 18 20 22 24 26
Million bp
b)
Chromosome XIX
fixed/variable SNPs
FST
SNP density
1.0
0.75
0.5
0.25
0
0 2 4 6 8 10 12 14 16
Million bp
5.0
2.5
0.0
-2.5
-5.0
fixed/variable SNPs
fraction of repetitive elements
SNP coverage
GC ratio
0 2 4 6 8 10 12 14 16
Million bp


Chr I
ORPM 30_1
ORPM 137
GCPM 124
ASP 112376
PMGC 2852
ASP 113302
GCPM 1719
Million bp
Chr II
Million bp
Chr III
GCPM 1133
ORPM 30_2
GCPM 1629
ORPM 203
GCPM 1869
GCPM 1688
Million bp
Chr IV
Million bp
Chr V
Million bp
Chr VI
GCPM 139
GCPM 1831
GCPM 1074
ORPM 26
ORPM 167
ASP 106933
ORPM 190
WPMS 12
GCPM 2034
ORPM 369
ORPM 60
GCPM 1065
ASP 112322
Million bp
Chr VII
Million bp
Chr VIII
Million bp
Chr IX
Million bp

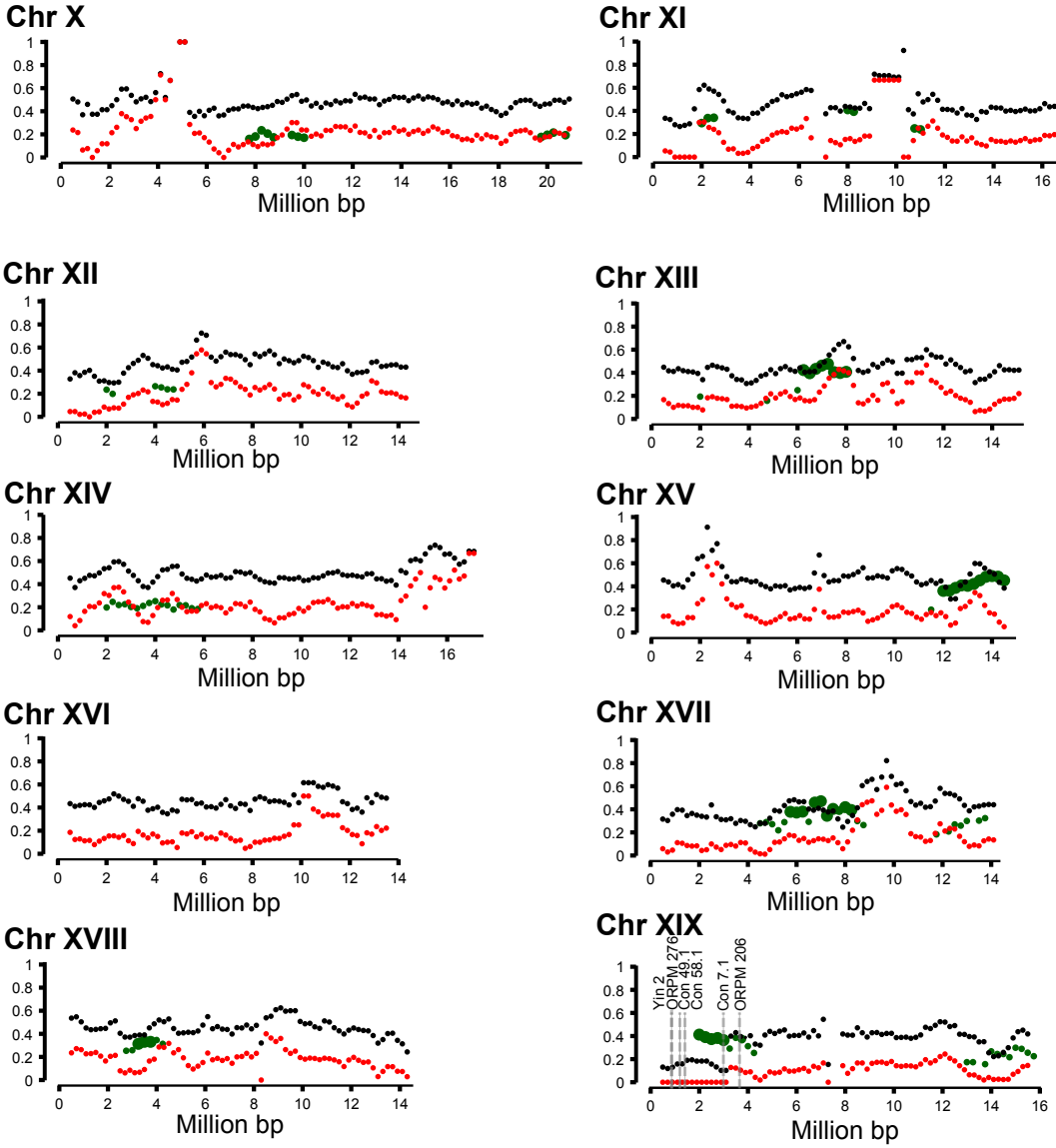

Chr X
Chr XI
Chr XII
Chr XIII
Chr XIV
Chr XV
Chr XVI
Chr XVII
Chr XVIII
Chr XIX
Million bp
Yin 2
ORPM 276
Con 49.1
Con 58.1
Con 7.1
ORPM 206

Table S1 RAD sequencing results

RAD sequencing results for 14 samples of *Populus alba* and *P. tremula.* Samples included in RAD sequencing ("**Ind**" column) have also been typed at 32 microsatellite loci. For each individual, the species ("**species**") is indicated, as are the number of Illumina sequencing reads ("**N reads**"), the number of unique sequence clusters ("**N cluster**"), the number of sequence clusters passing quality tests ("**Qual. Cluster**") and the median sequencing depth of each quality cluster ("**Med. seq. depth**"). We also indicate the average phred-quality of sequencing reads ("**Avg. Phred qual**.") and the total length of raw data per individual in million base pairs ("**Raw Seq. lgth (Mbp)**"). Where appropriate, sums and averages are indicated.

Ind	species	N reads	N cluster	Qual. Cluster	Med seq. depth	Avg. Phred qual	Raw Seq. lgth (Mbp)
I_273	*P. alba*	1'534'976	512'389	75'068	10	30.7	122.8
I_309	*P. alba*	1'631'688	381'381	82'327	11	30.7	130.5
I_318	*P. alba*	1'788'535	579'347	78'903	10	30.5	143.1
I_319	*P. alba*	2'394'469	927'726	86'702	11	30.1	191.6
I_324	*P. alba*	2'124'086	382'524	96'869	13	30.9	169.9
I_326	*P. alba*	1'597'571	282'022	87'320	12	31.1	127.8
I_363	*P. alba*	1'522'854	339'675	81'518	11	31.0	121.8
I_360	*P. tremula*	1'838'312	261'556	101'560	12	31.0	147.1
I_381	*P. tremula*	1'796'679	327'849	97'174	11	31.4	143.7
I_422	*P. tremula*	2'302'424	270'117	112'384	14	31.3	184.2
I_426	*P. tremula*	2'131'775	292'026	109'782	13	30.8	170.5
I_431	*P. tremula*	1'464'379	270'933	83'325	10	31.0	117.2
I_435	*P. tremula*	1'837'509	371'826	98'654	11	31.1	147.0
I_455	*P. tremula*	2'676'287	376'669	115'558	14	31.2	214.1
Σ	**14**	**26'641'544**	**5'576'040**	**1'307'144**	**-**	**-**	**2'131.3**
μ		**1'902'967**	**398'289**	**93'367**	**11.6**	**30.9**	**152.2**

Table S2 - Microsatellite markers

Thirty-two microsatellite loci ("**Locus**") with detailed information on genomic location of each marker ("**Chr**" = chromosome; "**Pos**" = location of the locus in base pairs on the chromsome). For each locus, the number of individuals scored is indicated for the Italian ("**N Italy**") and the Hungarian ("**N Hun**") hybrid zones along with information on the number of different alleles observed in each locality ("**$N_{Alleles}$ Italy**", "**$N_{Alleles}$ Hun**"). Allele frequency differentials between species are provided for each microsatellite locus in each hybrid zone ("**delta Italy**", "**delta Hun**").

Locus	Chr	Scoring	Pos	N Italy	$N_{Alleles}$ Italy	delta Italy	N Hun	$N_{Alleles}$ Hun	delta Hun
ORPM 30_1*	1	co-dominant	1'529'622.00	213	3	0.0547	185	6	0.2500
ORPM 137	1	co-dominant	9'087'453.00	210	10	0.9828	168	11	0.9011
GCPM 124	1	co-dominant	9'131'303.00	213	6	0.7917	172	7	0.8904
ASP 112376	1	co-dominant	13'305'812.00	214	15	0.9444	170	16	1.0000
PMGC 2852	1	co-dominant	14'548'286.00	216	21	0.7941	186	25	0.5478
ASP 113302	1	co-dominant	30'444'558.00	209	9	0.5776	170	13	0.6345
GCPM 1719	1	co-dominant	35'488'312.00	210	7	0.5812	171	11	0.6219
GCPM 1133	3	co-dominant	4'716'293.00	180	12	0.8713	131	8	0.5505
ORPM 30_2*	3	co-dominant	10'738'184.00	200	24	0.9063	184	26	0.5320
GCPM 1629	3	co-dominant	11'310'185.00	208	17	0.8026	144	20	0.9444
ORPM 203	3	co-dominant	12'009'782.00	215	6	0.4806	176	6	0.5119
GCPM 1869	3	co-dominant	16'805'774.00	217	20	1.0000	174	22	1.0000
GCPM 1688	3	co-dominant	17'574'314.00	212	8	0.8000	171	15	0.6497
GCPM 139	6	co-dominant	2'281'003.00	217	8	1.0000	184	11	1.0000
GCPM 1831	6	co-dominant	3'671'141.00	215	11	0.7319	182	13	0.5480
GCPM 1074	6	co-dominant	3'989'388.00	217	3	0.9922	182	2	0.9944
ORPM 26	6	co-dominant	5'786'927.00	218	6	0.7073	179	9	0.8315
ORPM 167	6	co-dominant	5'821'040.00	214	4	0.9605	184	5	0.9914
ASP 106933	6	co-dominant	13'019'647.00	214	10	1.0000	179	14	0.9890
ORPM 190	6	co-dominant	13'718'036.00	217	3	0.9634	184	3	0.9130
WPMS 12	6	co-dominant	19'471'676.00	175	10	0.9160	170	21	0.9382
GCPM 2034	6	co-dominant	22'219'025.00	215	12	0.9625	156	17	0.9643
ORPM 369	6	co-dominant	22'796'697.00	206	5	0.3525	178	6	0.2407
ORPM 60	6	co-dominant	23'655'126.00	214	10	0.6410	185	12	0.7513
GCPM 1065	6	co-dominant	24'119'014.00	210	7	0.8571	181	7	0.6218
ASP 112322	6	co-dominant	25'184'620.00	219	15	0.9878	166	18	0.8590
Yin 2	19	co-dominant	863'878.00	206	26	0.5710	168	27	0.3120
ORPM 276**	19	co-dominant	886'814.00	218	6	0.1856	179	7	0.1401
Con 49.1	19	co-dominant	1'220'062.00	182	8	0.7516	184	12	0.6908
Con 58.1	19	co-dominant	1'426'114.00	194	9	0.6389	159	11	0.7750
Con 7.1	19	co-dominant	2'978'082.00	188	8	0.2670	172	13	0.2479
ORPM 206	19	co-dominant	3'630'075.00	209	7	0.1154	186	12	0.6272

All primer combinations have been localized by blast-n searches against version 2 (build 156) of the *Populus trichocarpa* genome

* Primer combination ORPM 30 amplifies two separate loci in the genome, clearly distinct in allele sizes and chromosomal location. The two loci are denoted ORPM 30_1 and ORPM 30_2

** BLAST searches against *Populus trichocarpa* Version 2 (build 156) have identified a duplication of this locus. Here, we follow the notation of Macaya-Sanz et al 2011. A duplicate element is also located on chromosome 19, at position 2850207

Table S6 Genomic correlations

Pair-wise Pearson correlation coefficients between windowed (non-overlapping windows sized 100kb, Table S5) estimates of differentiation between the genomes of *P. alba* and *P. tremula*, and windowed genomic features affecting SNP distributions: average FST (**avgFST**), number of fixed SNPs (**fixed**), number of variable SNPs (**variable**), number of SNPs/100kb (**density**), proportion of fixed over informative SNPs (**fixratio**), fraction of repetitive DNA elements (**repfract**), ratio of GC basepairs (**gcratio**), and fraction of ambiguous (non-ACGT) basepairs (**xratio**).

	avgFST	**fixed**	**variable**	**density**	**fixratio**	**repfract**	**gcratio**
avgFST							
fixed	0.590**						
variable	-0.227**	0.255**					
density	-0.080**	0.442**	0.974**				
fixratio	0.734**	0.855**	-0.143**	0.047*			
repfract	0.019NS	-0.173**	-0.326**	-0.336**	-0.026NS		
gcratio	0.057*	0.217**	0.267**	0.296**	0.109**	-0.273**	
xratio	-0.083**	-0.202**	-0.188**	-0.214**	-0.120**	0.203**	-0.270**

****** indicates significant correlations with $p<0.001$, * indicates correlations with $0.01<p<0.05$, and **NS** indicates not significant correlations with $p>0.05$